=> d his

(FILE 'USPAT' ENTERED AT 10:11:34 ON 12 APR 1999)
ACTIVATE L879827/L

L1 (2)SEA FILE=USPAT APETALA?
L2 (478)SEA FILE=USPAT AP2 OR AP 2
L3 (141072)SEA FILE=USPAT PLANT#
L4 (61)SEA FILE=USPAT L2 AND L3
L5 (3)SEA FILE=USPAT APETALA?
L6 (65)SEA FILE=USPAT L2 AND L3
L7 (2145)SEA FILE=USPAT SEED#(3A)(MASS OR SIZE OR LARGER OR SMALLER
)
L8 (1834)SEA FILE=USPAT TRANSGENIC?
L9 (14)SEA FILE=USPAT L7 AND L8
L10 (1834)SEA FILE=USPAT TRANSGENIC?
L11 (14)SEA FILE=USPAT L7 AND L10

L12 11 S L5
L13 100 S L6
L14 26 S L9
=> d l12 1-8

1. 5,892,009, Apr. 6, 1999, DNA and encoded protein which regulates cold and dehydration regulated genes; Michael F. Thomashow, et al., 536/22.1; 530/350, 370, 379; 536/23.6; 800/278 [IMAGE AVAILABLE]

2. 5,891,859, Apr. 6, 1999, Method for regulating cold and dehydration regulatory genes in a plant; Michael F. Thomashow, et al., 514/44; 435/440; 530/350, 370, 379; 536/23.6; 800/278 [IMAGE AVAILABLE]

3. 5,861,542, Jan. 19, 1999, Gene controlling floral development and apical dominance in plants; Gynheung An, 435/69.1, 70.1, 320.1, 419; 536/23.6 [IMAGE AVAILABLE]

4. 5,859,338, Jan. 12, 1999, Plant clavata1 nucleic acids, transformed plants, and proteins; Elliot M. Meyerowitz, et al., 800/298; 435/69.1, 320.1, 419; 536/23.6; 800/290 [IMAGE AVAILABLE]

5. 5,859,326, Jan. 12, 1999, Gene controlling floral development and apical dominance in plants; Gynheung An, 800/290; 435/69.1, 70.1, 320.1, 419; 536/23.6, 24.3; 800/298, 317.3 [IMAGE AVAILABLE]

6. 5,844,119, Dec. 1, 1998, Genetically modified plants having modulated flower development; Detlef Weigel, 800/287; 435/69.1, 320.1, 419; 536/23.6, 24.1; 800/290, 298, 317.3 [IMAGE AVAILABLE]

7. 5,824,868, Oct. 20, 1998, Plants having modified response to ethylene; Elliot M. Meyerowitz, et al., 800/286; 435/320.1, 419; 536/23.6, 24.5; 800/283, 287, 298 [IMAGE AVAILABLE]

8. 5,811,536, Sep. 22, 1998, Cauliflower floral meristem identity genes and methods of using same; Martin F. Yanofsky, 536/23.6; 435/320.1, 419 [IMAGE AVAILABLE]
=> d l13 1-35

1. 5,892,009, Apr. 6, 1999, DNA and encoded protein which regulates cold and dehydration regulated genes; Michael F. Thomashow, et al., 536/22.1; 530/350, 370, 379; 536/23.6; 800/278 [IMAGE AVAILABLE]

2. 5,891,859, Apr. 6, 1999, Method for regulating cold and dehydration regulatory genes in a **plant**; Michael F. Thomashow, et al., 514/44; 435/440; 530/350, 370, 379; 536/23.6; 800/278 [IMAGE AVAILABLE]

3. 5,888,981, Mar. 30, 1999, Methods for regulating gene expression; Hermann Bujard, et al., 514/44; 424/93.21 [IMAGE AVAILABLE]

4. 5,888,768, Mar. 30, 1999, Compositions and methods for producing heterologous polypeptides in Pichia methanolica; Christopher K. Raymond, 435/69.1, 254.2, 320.1 [IMAGE AVAILABLE]

5. 5,885,829, Mar. 23, 1999, Engineering oral tissues; David J. Mooney, et al., 435/325; 424/49, 422, 435; 435/69.1, 374, 378 [IMAGE AVAILABLE]

6. 5,883,124, Mar. 16, 1999, Compositions and methods for treating and preventing pathologies including cancer; Dvorit Samid, 514/538, 557, 563, 567, 568, 570, 725 [IMAGE AVAILABLE]

7. 5,879,906, Mar. 9, 1999, Glucuronide repressors and uses thereof; Richard A. Jefferson, et al., 435/69.1, 91.41, 243, 320.1, 325, 410; 536/23.4, 23.5, 24.1 [IMAGE AVAILABLE]

8. 5,877,213, Mar. 2, 1999, Compositions and methods for therapy and prevention of cancer, AIDS, and anemia; Dvorit Samid, 514/568, 570 [IMAGE AVAILABLE]

9. 5,874,400, Feb. 23, 1999, Recombinant C140 receptor, its agonists and antagonists, and nucleic acids encoding the receptor; Johan Sundelin, et al., 514/2; 435/7.1, 7.2; 530/387.1, 388.1, 388.2, 391.3 [IMAGE AVAILABLE]

10. 5,872,206, Feb. 16, 1999, Compositions and methods for interfering wtih hepatitis B virus infection; Tsanyang Jake Liang, et al., 530/300,

324, 326, 350, 412 [IMAGE AVAILABLE]

11. 5,869,333, Feb. 9, 1999, Ryegrass pollen allergen; Mohan Bir Singh, et al., 435/325, 320.1; 536/23.6 [IMAGE AVAILABLE]

12. 5,867,588, Feb. 2, 1999, Method and apparatus for analyzing facial configurations and components; Stephen R. Marquardt, 382/118; 345/425, 435; 382/154, 254 [IMAGE AVAILABLE]

13. 5,866,755, Feb. 2, 1999, Animals transgenic for a tetracycline-regulated transcriptional inhibitor; Hermann Bujard, et al., 800/9, 18 [IMAGE AVAILABLE]

14. 5,861,542, Jan. 19, 1999, Gene controlling floral development and apical dominance in **plants**; Gynheung An, 435/69.1, 70.1, 320.1, 419; 536/23.6 [IMAGE AVAILABLE]

15. 5,859,326, Jan. 12, 1999, Gene controlling floral development and apical dominance in **plants**; Gynheung An, 800/290; 435/69.1, 70.1, 320.1, 419; 536/23.6, 24.3; 800/298, 317.3 [IMAGE AVAILABLE]

16. 5,859,310, Jan. 12, 1999, Mice transgenic for a tetracycline-controlled transcriptional activator; Hermann Bujard, et al., 800/9; 435/69.1, 70.1, 320.1, 325; 514/152; 536/23.4, 24.1; 800/4, 18, 22, 25 [IMAGE AVAILABLE]

17. 5,853,975, Dec. 29, 1998, Methods for identifying compositions for the treatment of body weight disorders, including obesity; Louis Anthony Tartaglia, 435/4, 29 [IMAGE AVAILABLE]

18. 5,844,119, Dec. 1, 1998, Genetically modified **plants** having modulated flower development; Detlef Weigel, 800/287; 435/69.1, 320.1, 419; 536/23.6, 24.1; 800/290, 298, 317.3 [IMAGE AVAILABLE]

19. 5,843,994, Dec. 1, 1998, Compositions and methods for treating and preventing pathologies including cancer; Dvorit Samid, 514/510, 513, 515, 529, 538, 563, 567 [IMAGE AVAILABLE]

20. 5,843,652, Dec. 1, 1998, Isolation and characterization of Agouti: a diabetes/obesity related gene; Richard P. Woychik, 435/6, 91.2; 536/23.1, 24.3, 24.33 [IMAGE AVAILABLE]

21. 5,843,643, Dec. 1, 1998, Site-specific transfection of eukaryotic cells using polypeptide-linked recombinant nucleic acid; Paul L. Ratner, 435/6, 5, 91.1; 514/2, 44; 530/300, 350; 536/23.1, 24.3, 24.5 [IMAGE AVAILABLE]

22. 5,840,316, Nov. 24, 1998, Ryegrass pollen allergen; Mohan Bir Singh, et al., 424/275.1, 184.1, 185.1, 276.1; 435/69.3; 530/370 [IMAGE AVAILABLE]

23. 5,837,486, Nov. 17, 1998, Method for preparing soluble analogues of integrins; Sarah C. Bodary, et al., 435/69.1, 69.7 [IMAGE AVAILABLE]

24. 5,834,242, Nov. 10, 1998, Human clathrin-associated protein; Olga Bandman, et al., 435/69.1, 320.1, 325; 536/23.1, 24.31 [IMAGE AVAILABLE]

25. 5,814,618, Sep. 29, 1998, Methods for regulating gene expression; Hermann Bujard, et al., 514/44; 424/93.21 [IMAGE AVAILABLE]

26. 5,811,536, Sep. 22, 1998, Cauliflower floral meristem identity genes and methods of using same; Martin F. Yanofsky, 536/23.6; 435/320.1, 419 [IMAGE AVAILABLE]

27. 5,811,403, Sep. 22, 1998, Polysaccharide toxin from Group B .beta.-hemolytic Streptococcus (GBS) having improved purity; Carl G. Hellerqvist, 514/23; 435/72, 253.4; 530/415; 536/6 [IMAGE AVAILABLE]

28. 5,804,194, Sep. 8, 1998, Vaccines containing a salmonella bacteria attenuated by mutation of the htra gene; Gordan Dougan, et al., 424/200.1, 93.2, 93.4, 235.1, 258.1 [IMAGE AVAILABLE]

29. 5,801,031, Sep. 1, 1998, Human and rat gamma glutamyl hydrolase genes; John Henry Galivan, et al., 435/6, 69.1, 195, 320.1, 325, 353, 366, 372; 536/23.1, 23.2, 23.5, 24.31 [IMAGE AVAILABLE]

30. 5,792,850, Aug. 11, 1998, Hematopoietic cytokine receptor; James W. Baumgartner, et al., 536/23.5; 435/69.5, 335 [IMAGE AVAILABLE]

31. 5,789,651, Aug. 4, 1998, Isolation and characterization of Agouti: a diabetes/obesity related gene; Richard P. Woychik, 800/9; 435/69.1, 91.2, 320.1; 536/23.1; 800/10, 18, 25 [IMAGE AVAILABLE]

32. 5,789,156, Aug. 4, 1998, Tetracycline-regulated transcriptional inhibitors; Hermann Bujard, et al., 435/6, 69.1, 69.7, 252.3, 320.1, 810; 536/23.4, 23.7, 24.1 [IMAGE AVAILABLE]

33. 5,776,759, Jul. 7, 1998, Two novel human cathepsin proteins; Olga Bandman, et al., 435/226, 252.3, 254.11, 320.1, 325; 536/23.2, 24.31 [IMAGE AVAILABLE]

34. 5,776,234, Jul. 7, 1998, Anionic bituminous emulsions with improved adhesion; Peter Schilling, 106/277, 278, 284.06 [IMAGE AVAILABLE]

35. 5,772,749, Jun. 30, 1998, Anionic bituminous emulsions with improved adhesion; Peter Schilling, et al., 106/277, 284.4; 524/61 [IMAGE AVAILABLE]
=> d l14 1-12

1. 5,880,331, Mar. 9, 1999, Use of anthocyanin genes to maintain male sterile plants; Enno Krebbers, et al., 47/DIG.1; 536/24.1, 27.1 [IMAGE AVAILABLE]

2. 5,866,763, Feb. 2, 1999, Inbred corn line ZS01220; Michael B. Buendgen, 800/300.1; 47/DIG.1; 435/412, 424, 430, 430.1; 800/271, 275, 279, 281, 284, 301, 302, 320.1 [IMAGE AVAILABLE]

3. 5,859,338, Jan. 12, 1999, Plant clavata1 nucleic acids, transformed plants, and proteins; Elliot M. Meyerowitz, et al., 800/298; 435/69.1, 320.1, 419; 536/23.6; 800/290 [IMAGE AVAILABLE]

4. 5,856,452, Jan. 5, 1999, Oil bodies and associated proteins as affinity matrices; Maurice Moloney, et al., 530/412; 435/262, 270, 272, 277 [IMAGE AVAILABLE]

5. 5,855,881, Jan. 5, 1999, Mammalian alcohol dehydrogenase and aldehyde dehydrogenase production in plants; John D. Loike, et al., 424/94.2; 435/190; 514/2 [IMAGE AVAILABLE]

6. 5,850,028, Dec. 15, 1998, Soybean cultivar CX205; Nancy Anne Sebern, 800/312; 435/415, 426, 430; 800/260 [IMAGE AVAILABLE]

7. 5,850,016, Dec. 15, 1998, Alteration of amino acid compositions in seeds; Rudolf Jung, et al., 800/287; 435/6, 69.1, 320.1, 410, 415; 536/23.1, 23.4, 23.6; 800/312 [IMAGE AVAILABLE]

8. 5,824,863, Oct. 20, 1998, Seed coat-specific cryptic promoter in tobacco; Brian Miki, et al., 800/298; 435/69.1, 320.1, 418, 419; 536/24.1; 800/287, 317.3 [IMAGE AVAILABLE]

9. 5,801,026, Sep. 1, 1998, Use of plant fatty acyl hydroxylases to produce hydroxylated fatty acids and derivatives in plants; Chris Somerville, et al., 800/281; 435/134; 530/377; 536/23.6 [IMAGE AVAILABLE]

10. 5,773,697, Jun. 30, 1998, Genetic constructs and methods for producing fruits with very little or diminished seed; Dwight T. Tomes, et al., 800/260; 435/69.1, 320.1; 536/23.7, 24.1; 800/268, 287, 290, 298, 308, 309 [IMAGE AVAILABLE]

11. 5,773,693, Jun. 30, 1998, Pea ADP-glucose pyrophosphorylase subunit genes and their uses; Diane G. Burgess, et al., 800/284; 435/69.1, 100, 101, 194; 536/23.6; 800/298 [IMAGE AVAILABLE]

12. 5,773,691, Jun. 30, 1998, Chimeric genes and methods for increasing the lysine and threonine content of the seeds of plants; Saverio Carl Falco, et al., 800/287; 435/69.1, 119, 320.1; 536/23.1, 23.6, 23.7, 24.1; 800/298, 306, 312, 320.1 [IMAGE AVAILABLE]
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95% OF LIMIT FOR SAVED L# LISTS REACHED
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SESSION WILL BE HELD FOR 30 MINUTES
U.S. Patent & Trademark Office SESSION SUSPENDED AT 10:28:39 ON 12 APR 199

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 * * * * * * RECONNECTED TO U.S. Patent & Trademark Office * * * * * *
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FILE 'USPAT' ENTERED AT 07:22:33 ON 22 JUN 1998
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L1 (       2)SEA FILE=USPAT APETALA?
L2 (     478)SEA FILE=USPAT AP2 OR AP 2
L3 (  141072)SEA FILE=USPAT PLANT#
L4 (      61)SEA FILE=USPAT L2 AND L3
=> s l1
L5         3 APETALA?
=> d 1
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1. 5,744,693, Apr. 28, 1998, Plants having altered floral development; Elliot M. Meyerowitz, et al., 800/205; 435/172.3, 320.1; 800/DIG.15, DIG.17, DIG.43 [IMAGE AVAILABLE]

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=> d his

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         DEL HIS
         ACTIVATE L700152/L
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L1 (       2)SEA FILE=USPAT APETALA?
L2 (     478)SEA FILE=USPAT AP2 OR AP 2
L3 (  141072)SEA FILE=USPAT PLANT#
L4 (      61)SEA FILE=USPAT L2 AND L3
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L5         3 S L1
=> s l4
       315 AP2
      9525 AP
   2297700 2
       192 AP 2
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    142918 PLANT#
L6        65 L2 AND L3
=> d 1-4
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1. 5,767,363, Jun. 16, 1998, **Plant** promoter involved in controlling lipid biosynthesis in seeds; Jacqueline De Silva, et al., 800/205; 435/70.1, 172.3, 320.1; 536/24.1; 800/255, DIG.15, DIG.16, DIG.17 [IMAGE AVAILABLE]

2. 5,763,575, Jun. 9, 1998, Agonist and antagonist peptides of the C140 receptor; Johan Sundelin, et al., 530/327, 300, 328, 329, 330 [IMAGE AVAILABLE]

3. 5,763,218, Jun. 9, 1998, Nucleic acid encoding novel human G-protein coupled receptor; Ryo Fujii, et al., 435/69.1, 252.3, 254.11, 320.1, 325; 536/23.5 [IMAGE AVAILABLE]

4. 5,759,812, Jun. 2, 1998, Human selenium-binding protein; Olga Bandman, et al., 435/69.2, 71.1, 252.33, 320.1; 536/23.1, 23.5, 24.31, 24.5 [IMAGE AVAILABLE]

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=> s seed#(3a)(mass or size or larger or smaller)
     49480 SEED#
    292141 MASS
    853715 SIZE
    635357 LARGER
    591471 SMALLER
L7      2145 SEED#(3A)(MASS OR SIZE OR LARGER OR SMALLER)
=> s transgenic?
L8      1834 TRANSGENIC?
=> s l7 and l8
L9        14 L7 AND L8
=> d 1-14
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1. 5,767,363, Jun. 16, 1998, Plant promoter involved in controlling lipid biosynthesis in seeds; Jacqueline De Silva, et al., 800/205; 435/70.1, 172.3, 320.1; 536/24.1; 800/255, DIG.15, DIG.16, DIG.17 [IMAGE AVAILABLE]

2. 5,750,867, May 12, 1998, Maintenance of male-sterile plants; Mark Williams, et al., 800/205; 47/58, DIG.1; 435/172.3, 199, 418, 419; 536/23.2, 23.6, 23.7, 24.1; 800/250, DIG.56 [IMAGE AVAILABLE]

3. 5,668,292, Sep. 16, 1997, Use of plant fatty acyl hydroxylases to produce hydroxylated fatty acids and derivatives in plants; Chris Somerville, et al., 800/205; 435/172.1; 530/377; 536/23.6; 800/DIG.69 [IMAGE AVAILABLE]

4. 5,658,772, Aug. 19, 1997, Site-specific recombination of DNA in plant cells; Joan Tellefsen Odell, et al., 435/172.3, 69.1, 172.1, 320.1, 410, 418, 419; 536/23.74; 800/205; 935/34 [IMAGE AVAILABLE]

5. 5,650,554, Jul. 22, 1997, Oil-body proteins as carriers of high-value peptides in plants; Maurice Moloney, 800/205; 435/69.1, 69.2, 69.52, 69.6, 69.7, 69.8, 70.1, 71.1, 172.3, 183, 320.1, 418, 419; 536/23.2, 23.4, 23.52, 23.6, 24.1; 800/250, DIG.15 [IMAGE AVAILABLE]

6. 5,639,948, Jun. 17, 1997, Stamen-specific promoters from rice; Frank Michiels, et al., 800/205; 47/58, DIG.1; 435/172.1, 172.3, 414, 419; 536/23.2, 23.6, 24.1; 935/35, 36, 67 [IMAGE AVAILABLE]

7. 5,633,440, May 27, 1997, P119 promoters and their uses; Pamela

Dunsmuir, et al., 800/205; 435/172.3, 320.1; 536/23.6, 24.1; 800/DIG.40, DIG.43, DIG.44 [IMAGE AVAILABLE]

8. 5,623,067, Apr. 22, 1997, Seed-specific promoter region; Joel S. Vandekerckhove, et al., 536/24.1; 435/172.3, 320.1; 800/205 [IMAGE AVAILABLE]

9. 5,589,617, Dec. 31, 1996, Enhanced regeneration system; Narender S. Nehra, et al., 800/205; 435/172.3, 430.1; 800/255, DIG.52, DIG.58; 935/52 [IMAGE AVAILABLE]

10. 5,506,136, Apr. 9, 1996, Method for regeneration of coniferous plants by somatic embryogenesis; Michael R. Becwar, et al., 435/422 [IMAGE AVAILABLE]

11. 5,498,831, Mar. 12, 1996, Pea ADP-glucose pyrophosphorylase subunit genes and their uses; Diane G. Burgess, et al., 800/205; 435/100, 172.1, 172.3, 194, 430; 536/23.2, 23.6, 24.5; 800/200, 250, 255, DIG.23 [IMAGE AVAILABLE]

12. 5,487,991, Jan. 30, 1996, Process for the production of biologically active peptide via the expression of modified storage seed protein genes in **transgenic** plants; Joel S. Vandekerckhove, et al., 435/172.3, 69.1; 530/377; 536/23.4, 23.5, 23.51, 23.6; 800/205, 250, DIG.70; 935/64 [IMAGE AVAILABLE]

13. 5,477,000, Dec. 19, 1995, Hyperproduction of shoots during a vitro regeneration of plant; Praveen K. Saxena, et al., 435/430; 47/58; 435/430.1 [IMAGE AVAILABLE]

14. 5,413,930, May 9, 1995, Method for regeneration of coniferous plants by somatic embryogenesis; Michael R. Becwar, et al., 435/422 [IMAGE AVAILABLE]

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75% OF LIMIT FOR SAVED L# LISTS REACHED
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SESSION WILL BE HELD FOR 30 MINUTES
U.S. Patent & Trademark Office SESSION SUSPENDED AT 07:52:51 ON 22 JUN 199

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$0.89 Estimated cost File351
$0.89 Estimated cost this search
$0.89 Estimated total session cost 0.091 DialUnits

File 5:BIOSIS PREVIEWS(R) 1969-1998/JUN W3
(c) 1998 BIOSIS

Set Items Description
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? s transgenic?
S1 22759 TRANSGENIC?
? s seed
S2 85262 SEED
? s mass
S3 187721 MASS
? s s1 and s2 and s3
22759 S1
85262 S2
187721 S3
S4 6 S1 AND S2 AND S3
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4/7/1
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1998 BIOSIS. All rts. reserv.
14171551 BIOSIS Number: 01171551
Morphological alterations and root nodule formation in Agrobacterium rhizogenes-mediated transgenic hairy roots of peanut (Arachis hypogaea L.)
Akasaka Y; Mii M; Daimon H
Dep. Plant Sci., Coll. Agric., Osaka Prefecture Univ., Sakai, Osaka 593, Japan
Annals of Botany (London) 81 (2). 1998. 355-362.
Full Journal Title: Annals of Botany (London)
ISSN: 0305-7364
Language: ENGLISH
Print Number: Biological Abstracts Vol. 105 Iss. 008 Ref. 114263
Transformed hairy roots were induced at the excised site of the epicotyl of dry mature seed of a Spanish type peanut (Arachis hypogaea) cv. Java 13 2 weeks after inoculation with a wild type strain of Agrobacterium rhizogenes, MAFF-02-10266. Composite plants consisting of transformed roots with non-transformed shoots were cultured using pouches. Forty days after inoculation, the composite plant showed a root system with abundant root mass, more lateral branching and high fractal dimension compared to the control. No differences were observed in production of rosette-type root hairs or the cross sectional structure between transformed and non-transformed roots. The inoculation of Bradyrhizobium sp. A2R1 strain to the composite plants led to the induction of transformed root nodules. These transformed root nodules showed production of leghaemoglobin in the bacterial zone and nitrogenase activity as assayed by C-2H-2 reduction, and exhibited enlargement of the nodule cortex region and de novo root formation from the nodule cortex.

4/7/2
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1998 BIOSIS. All rts. reserv.
13503241 BIOSIS Number: 99503241
Accumulation of ricinoleic, lesquerolic, and densipolic acids in seeds of transgenic arabidopsis plants that express a fatty acyl hydroxylase cDNA from castor bean
Broun P; Somerville C
Carnegie Inst. Washington, Dep.. Plant Biol., 290 Panama St., Stanford, CA 94305, USA
Plant Physiology (Rockville) 113 (3). 1997. 933-942.
Full Journal Title: Plant Physiology (Rockville)
ISSN: 0032-0889
Language: ENGLISH
Print Number: Biological Abstracts Vol. 103 Iss. 010 Ref. 142079
A cDNA encoding the oleate 12-hydroxylase from castor bean (Ricinus communis L.) has previously been shown to direct the synthesis of small amounts of ricinoleic acid (12-hydroxyoctadeccis-9-enoic acid) in seeds of transgenic tobacco plants. Expression of the cDNA under control of the Brassica napus napin promoter in transgenic Arabidopsis thaliana plants resulted in the accumulation of up to 17% of seed fatty acids as ricinoleate and two novel fatty acids that have been identified by gas chromatography-mass spectrometry as lesquerolic (14-hydroxyeicos-cis-11-eno ic acid) and densipolic (12-hydroxyoctadec-cis-9,15-dienoic acid) acids. Traces of auricolic acid were also observed. These results suggest that either the castor hydroxylase can utilize oleic acid and eicosenoic acid as substrates for ricinoleic and lesquerolic acid biosynthesis, respectively, or Arabidopsis contains an elongase that accepts ricinoleic acid as a substrate. These observations are also consistent with indirect biochemical evidence that an n-3 desaturase is capable of converting ricinoleic acid to densipolic acid. Expression of the castor hydroxylase also caused enhanced accumulation of oleic acid and a corresponding decrease in the levels of polyunsaturated fatty acids. Since the steady-state level of mRNA for the oleate-12 desaturase was not affected, it appears that the presence of the hydroxylase, directly or indirectly, causes posttranscriptional inhibition of desaturation.

4/7/3
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

13094190 BIOSIS Number: 99094190
Differential seed maturation uncouples fertilization and siring success in Oenothera organensis (Onagraceae)
Havens K; Delph L F
Missouri Botanical Garden, PO Box 299, St. Louis, MO 63166, USA
Heredity 76 (6). 1996. 623-632.
Full Journal Title: Heredity
ISSN: 0018-067X
Language: ENGLISH
Print Number: Biological Abstracts Vol. 102 Iss. 004 Ref. 059639
This study examines ovule fertilization and seed maturation success in an evening primrose, Oenothera organensis, using transgenic plants. The reproductive success of several pollen donors was compared using individuals transformed with the GUS (beta-glucuronidase) marker gene which allowed the genotype of developing ovules to be determined prior to seed abortion. This marker gene allowed us to discriminate between a pollen donor's success in fertilizing ovules and its success in siring seeds. Transformed plants had decreased microgametophytic vigour, as evidenced by lower than expected fertilization success in vivo and slower pollen tube growth rates in vitro. However, transformation had no apparent effect on offspring sporophytic vigour, including seed mass, seedling emergence and dry weight. This illustrates the effectiveness of fertilization competition in screening out poorly functioning haploid genomes as suggested by Mulcahy (1979). We found significant differences between the percentage of ovules fertilized and the percentage of seeds sired by a pollen donor in four of eight cases. Hence, fertilization success does not always predict seed paternity. The proportion of seeds sired by the transformed donor with very low fertilization success increased, whereas the proportion sired by the donor with relatively high fertilization success was reduced. This resulted in nearly equal siring ability for the two donors in spite of their difference in fertilization ability.

4/7/4
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

12033020 BIOSIS Number: 98633020
Lysophosphatidic acid acyltransferase from meadowfoam mediates insertion of erucic acid at the sn-2 position of triacylglycerol in transgenic rapeseed oil
Lassner M W; Levering C K; Davies H M; Knutzon D S
Calgene Inc., 1920 Fifth St., Davis, CA 95616, USA
Plant Physiology (Rockville) 109 (4). 1995. 1389-1394.
Full Journal Title: Plant Physiology (Rockville)
ISSN: 0032-0889
Language: ENGLISH
Print Number: Biological Abstracts Vol. 101 Iss. 004 Ref. 048765
Lysophosphatidic acid acyltransferase acylates the sn-2 hydroxyl group of lysophosphatidic acid to form phosphatidic acid, a precursor to triacylglycerol. A cDNA encoding lysophosphatidic acid acyltransferase was isolated from developing seeds of meadowfoam (Limnanthes alba alba). The cDNA encodes a 281 -amino acid protein with a molecular mass of 32 kD. The cDNA was expressed in developing seeds of transgenic high-erucic-acid rapeseed (Brassica napus) using a napin expression cassette. Erucic acid was present at the sn-2 position of triacylglycerols from transgenic plants but was absent from that position of seed oil extracted from control plants. Trierucin was present in the transgenic oil. Alteration of the sn-2 erucic acid composition did not affect the total erucic acid content. These experiments demonstrate the feasibility of using acyltransferases to alter the stereochemical composition of transgenic seed oils and also represent a necessary step toward increasing the erucic acid content of rapeseed oil.

4/7/5
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

7635927 BIOSIS Number: 90003927
PEA CONVICILIN STRUCTURE AND PRIMARY SEQUENCE OF THE PROTEIN AND EXPRESSION OF A GENE IN THE SEEDS OF TRANSGENIC TOBACCO
NEWBIGIN E J; DELUMEN B O; CHANDLER P M; GOULD A; BLAGROVE R J; MARCH J F
; KORTT A A; HIGGINS T J V
CSIRO DIV. PLANT INDUSTRY, GPO BOX 1600, CANBERRA, A.C.T. 2601, AUST.
PLANTA (HEIDELB) 180 (4). 1990. 461-470. CODEN: PLANA
Language: ENGLISH
Convicilin, a trimeric globulin of pea (Pisum sativum L.) seeds, is closely related to vicilin and composed of polypeptides of 68.2 kilodaltons. A partial copy DNA (cDNA) clone encoding convicilin was isolated, sequenced, and used to select a convicilin gene from a pea genomic library. A part of the genomic clone was sequenced to obtain the coding sequences missing in the cDNA clone and a further 1 kilobase 5' to the start of transcription were also obtained. The entire sequence of convicilin was deduced from the combined genomic and cDNA sequences. The complete gene encoding convicilin was transferred to tobacco (Nicotiana tabacum L.) and the characteristics of its expression in the seeds of transgenic plants were studied. An unprocessed polypeptide, which was found only in the seeds of the transgenic plants, was identical in size to pea convicilin, and was recognized by vicilin antibodies. Convicilin, which does not undergo posttranslational cleavage in peas, was partially processed to polypeptides of a relative molecular mass (Mr) of approx. 50,000 in transgenic tobacco seeds. There was a a twofold variation in the level of convicilin accumulated by the mature seeds of a number of transgenic plants and this was well correlated with the number of gene

copies incorporated in the different transformants. In the seeds of tobacco plants that contained a single copy of the transferred gene it was estimated that convicilin comprised up to 2% of the seed protein. Thus, using a combination of gene sequencing and expression in a heterologous host we believe we have characterized the gene corresponding to the Cvc locus, whereas the gene described by D. Bown et al. (1988, Biochem J., 251, 717-726) probably encodes a minor convicilin-related protein.

4/7/6
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1998 BIOSIS. All rts. reserv.
6450926 BIOSIS Number: 85051447
EXPRESSION OF THE BETA-SUBUNIT OF BETA CONGLYCININ IN SEEDS OF TRANSGENIC
PLANTS
BRAY E A; NAITO S; PAN N-S; ANDERSON E; DUBE P; BEACHY R N
DEP. BOT. AND PLANT SCI., UNIV. CALIF., RIVERSIDE, CALIF. 92521, USA.
PLANTA (BERL) 172 (3). 1987. 364-370. CODEN: PLANA
Full Journal Title: PLANTA (Berlin)
Language: ENGLISH
Soybean (Glycine max (L.) Merr.) seeds contain the storage protein .beta.-conglycinin, encoded by a multigene family. .beta.-Conglycinin consists of three subunits; .alpha.', .alpha., and .beta.. A genomic clone for a .beta.-subunit of .beta.-conglycinin has been characterized by restriction-enzyme mapping and hybrid selected in-vitro translation followed by immunoprecipitation. In order to determine the developmental regulation of this .beta.-subunit gene, its expression was studied in seeds of transgenic petunia (Petunia hybrida) and tobacco (Nicotiana tabacum L.) plants. The .beta.-subunit expressed in seeds of petunia and tobacco was recognized by anti-.beta.-conglycinin serum at a relative molecular mass of 53,000, equivalent to that of the native protein. Separation of the petunia-seed protein by isolelectric focusing following by sodium dodecyl sulfate-polyacrylamide gel electrophoresis and immunoblot analysis showed that multiple isoelectric forms of the .beta.-subunit were produced. There was approximately a twofold variation in the accumulation of the .beta.-subunit protein in the mature seeds of transgenic petunia plants, each containing a single .beta.-subunit gene. However, the level of protein accumulation in mature seeds and the amount of .beta.-subunit mRNA in developing seeds was not correlated. Accumulation of the .beta.-subunit protein in transgenic petunia seeds was less than the .alpha.'-subunit protein that accumulated in transgenic petunia seeds containing a single .alpha.'-subunit gene and less than the amount of the .beta.-subunit in mature soybean seeds which contain 8-13 .beta.-subunit genes. In transgenic tobacco plants, the accumulation of the .beta.-subunit protein in seeds was generally well correlated with the number of genes that were incorporated in the different transformants.
? ds

Set Items Description
S1 22759 TRANSGENIC?
S2 85262 SEED
S3 187721 MASS
S4 6 S1 AND S2 AND S3
? s larger or smaller
114631 LARGER
94046 SMALLER
S5 189675 LARGER OR SMALLER
? s seed or seeds
85262 SEED
53765 SEEDS
S6 113089 SEED OR SEEDS
? s s1 and s3 and s6 not s4
22759 S1
187721 S3
113089 S6
6 S4
S7 6 S1 AND S3 AND S6 NOT S4
? t s7/7/1-6

7/7/1
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1998 BIOSIS. All rts. reserv.
13542057 BIOSIS Number: 99542057
The application of biotechnology to agricultural production
Lin C-Y; Wang C-S; Wang H-L; Chen L-J; Tsay H-S
Taiwan Agric. Res. Inst., Natl. Chung-Hsing Univ., Taichung, Taiwan
Journal of the Agricultural Association of China 0 (176). 1996. 11-37.
Full Journal Title: Journal of the Agricultural Association of China
ISSN: 0300-550X
Language: CHINESE
Print Number: Biological Abstracts Vol. 103 Iss. 012 Ref. 165485
The rapid development of biotechnology in recent years has contributed greatly to the advancement of plant sciences. Its application can be categorized into two fields, i.e., tissue culture and molecular biology. This paper summarizes the application of biotechnology to crop production with representing examples. A. Tissue culture 1. The combination of meristem/shoot-tip culture and heat treatment for the production of virus-free seedlings. 2. Techniques of tissue culture and suspension culture for the preservation of plant germplasms. 3. The overcome of cross incompatibility between distantly-related species by test-tube fertilization and embryo rescue for the production of disease-and insect-resistant cultivars. 4. The improvement of breeding efficiency by the utilization of haploid plants from anther culture. 5. The utilization of liquid suspension culture for mass propagation, mutation breeding, and the production of artificial seeds and secondary products. 6. The

production of somatic hybrids and materials for genetic engineering studies by protoplast culture and fusion. B. Molecular biology 1. The development of cultivars with new flower colors. 2. The establishment of genetic map and gene isolation. 3. The regulation of gene via antisense genes. 4. The detection and identification of viruses in plants. 5. The production of disease-and insect-resistant plants through gene manipulation. 6. The production of animals and human vaccines from transgenic plants.

7/7/2
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

13254316 BIOSIS Number: 99254316
Rice allergenic protein and molecular-genetic approach for hypoallergenic rice
Nakamura R; Matsuda T
Dep. Applied Biol. Sci., Sch. Agricultural Sci., Nagoya Univ., Chikusa, Nagoya 464-01, Japan
Bioscience Biotechnology and Biochemistry 60 (8). 1996. 1215-1221.
Full Journal Title: Bioscience Biotechnology and Biochemistry
ISSN: 0916-8451
Language: ENGLISH
Print Number: Biological Abstracts Vol. 102 Iss. 011 Ref. 169946
Allergenic proteins with a molecular mass of about 14 to 16 kDa were isolated from a rice salt-soluble fraction based on the reactivity with IgE antibodies from patients allergic to rice. cDNA clones encoding these allergenic proteins were isolated from a cDNA library of maturing rice seeds, and the deduced amino acid sequences showed considerable similarity to wheat and barley alpha-amylase/trypsin inhibitors, which have recently been identified as major allergens associated with baker's asthma. An antisense RNA strategy was applied to repress the allergen gene expression in maturing rice seeds. Immunoblotting and ELISA analyses of the seeds using a monoclonal antibody to a 16-kDa allergen showed that allergen content of seeds from several transgenic rice plants was markedly lower than that of the seeds from parental wild type rice.

7/7/3
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

13012025 BIOSIS Number: 99012025
Transgenic tobacco plants expressing the Arabidopsis thaliana nitrilase II enzyme
Schmidt R-C; Mueller A; Hain R; Bartling D; Weiler E W
Lehrstuhl Pflanzenphysiol., Ruhr-Universitaet, Fakultaet Biologie, D-44780 Bochum, Germany
Plant Journal 9 (5). 1996. 683-691.
Full Journal Title: Plant Journal
ISSN: 0960-7412
Language: ENGLISH
Print Number: Biological Abstracts Vol. 102 Iss. 001 Ref. 012025
Nitrilase (E.C. 3.5.5.1) cloned from Arabidopsis thaliana converts indole-3-acetonitrile to the plant growth hormone, indole-3-acetic acid in vitro. To probe the capacity of this enzyme under physiological conditions in vivo, the cDNA PM255, encoding nitrilase II, was stably integrated into the genome of Nicotiana tabacum by direct protoplast transformation under the control of the CaMV-35S promotor. The regenerated plants appeared phenotypically normal. Nitrilase II was expressed, based on the occurrence of its mRNA and polypeptide. The enzyme was catalytically active, when extracted from leaf tissue of transgenic plants (specific activity: 25 fkat mg-1 protein with indole-3-acetonitrile as substrate). This level of activity was lower than that found in A. thaliana, and this was deemed essential for the in vivo analysis. Leaf tissue from the transgenic plants converted 1-(13C)-indole-3-acetonitrile to 1-(13C)-indole-3-acetic acid in vivo as determined by HPLC/GC-MS analysis. Untransformed tobacco was unable to catalyze this reaction. When transgenic seeds were grown on medium in the absence of indole-3-acetonitrile, germination and seedling growth appeared normal. In the presence of micromolar levels of exogenous indole-3-acetonitrile, a strong auxin-overproducing phenotype developed resulting in increased lateral root formation (at 10 mu-M indole-3-acetonitrile) or stunted shoot growth, excessive lateral root initiation, inhibition of root outgrowth and callus formation at the root/shoot interface (at 100 mu-M indole-3-acetonitrile). Collectively, these data prove the ability of nitrilase II to convert low micromolar levels of indole-3-acetonitrile to indole-3-acetic acid in vivo, even when expressed at subphysiological levels thereby conferring a high-auxin phenotype upon transgenic plants. Thus, the A. thaliana nitrilase activity, which exceeds that of the transgenic plants, would be sufficient to meet the requirements for auxin biosynthesis in vivo.

7/7/4
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

12032813 BIOSIS Number: 98632813
Nitrite reductase silencing as a tool for selecting spontaneous haploid plants
Vaucheret H; Mourrain P; Robalo J-C; Pollien J-M
Lab. Biol. Cellulaire, INRA, F-78026 Versailles Cedex, France
Plant Cell Reports 15 (1-2). 1995. 12-16.
Full Journal Title: Plant Cell Reports
ISSN: 0721-7714
Language: ENGLISH
Print Number: Biological Abstracts Vol. 101 Iss. 004 Ref. 048558
Using tobacco as a model species, we have developed a simple procedure for the selection of spontaneous haploid plants under horticultural conditions, which does not require the use of any selective agent. One

transgenic tobacco plant, homozygous for an antisense transgene able to silence the expression of nitrite reductase host genes, and encoding the second enzyme of the nitrate assimilation pathway, was used to pollinate two different cultivars of wild type tobacco plants. Seeds were sown at high density in the greenhouse and watered with a nutrient solution containing nitrate. Green plants able to develop normally emerged at a frequency of 5.10-4 in a mass of chlorotic retarded plants. Phenotypic and genetic analysis, chloroplast counting in stomatal guard cells and molecular hybridizations revealed that 22% of these plants were gynogenetic haploid plants exhibiting the maternal phenotype whereas the remaining 78% were true diploid plants that have lost the antisense transgene. These results demonstrate that a transgene able to silence the expression of a housekeeping gene can be utilized as a counter-selectionable marker for the rapid and easy selection of spontaneous haploid plants in transformable species.

7/7/5
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

11898865 BIOSIS Number: 98498865
An Arabidopsis mutant deficient in sterol biosynthesis: Heterologous complementation by ERG 3 encoding a DELTA-7-sterol-C-5-desaturase from yeast
Gachotte D; Meens R; Benveniste P
Dep. d'Enzymol. Mol. Cell., UPR, 406 du CNRS, 28 rue Goethe, 67084 Strasbourg, France
Plant Journal 8 (3). 1995. 407-416.
Full Journal Title: Plant Journal
ISSN: 0960-7412
Language: ENGLISH
Print Number: Biological Abstracts Vol. 100 Iss. 010 Ref. 149722
The mutant STE 1 was isolated by screening an ethylmethane sulfonate (EMS)-mutagenized population of Arabidopsis thaliana which consisted of 22 000 M-2 plants divided into 1100 pools of 20 plants by gas chromatography of sterols extracted from small leaf samples. STE 1 was characterized by the accumulation of three A7-sterols concomitantly with the decrease of the three corresponding DELTA-5-sterols which are the end products of the sterol pathway in wild-type leaves. The structure of these Al-sterols was determined after two steps of purification on HPLC, by gas chromatography coupled with mass spectrometry (GC-MS) and proton nuclear magnetic resonance spectrometry (1H-NMR). The accumulation of DELTA-7-sterols suggested that the mutant is deficient in the activity of the DELTA-7-sterol-C-5-desaturase. Genetic analysis showed that the accumulation of DELTA-7-sterols was due to a single recessive nuclear mutation. The mutant line STE 1 was backcrossed four times to the wild-type. The resulting STE 1 plants had wild-type morphology and set seeds normally, suggesting that the DELTA-7-sterols in STE 1 are good surrogates of physiologically active DELTA-5-sterols to sustain normal development. STE 1 roots were transformed with the Saccharomyces cerevisiae ERG 3 gene encoding the DELTA-7-sterol-C-5-desaturase under the control of the CaMV 35S promoter. Seven transgenic STE 1 root-derived calli showed an increase in DELTA-5-sterols and a concomitant decrease in Al-sterols in comparison with STE 1 untransformed root-derived calli. Northern blot analysis using the ERG 3 probe showed a strong expression of ERG 3 in three of the seven transgenic calli. These results suggest that the accumulation of DELTA-7-sterols in the STE 1 mutant is due to a deficiency of the DELTA-7-sterol-C-5-desaturation step in the plant sterol biosynthesis pathway.

7/7/6
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

10131113 BIOSIS Number: 95131113
EXPRESSION OF A CYSTEINE PROTEINASE INHIBITOR ORYZACYSTATIN I IN
TRANSGENIC TOBACCO PLANTS
MASOUD S A; JOHNSON L B; WHITE F F; REECK G R
PLANT BIOLOGY DIV., SAMUEL ROBERTS NOBLE FOUNDATION, P.O. BOX 2180,
ARDMORE, OK 73402.
PLANT MOL BIOL 21 (4). 1993. 655-663. CODEN: PMBID
Full Journal Title: Plant Molecular Biology
Language: ENGLISH
Expression of cysteine proteinase inhibitors (cystatins) in tobacco or other plants has the potential for improving resistance against pathogens and insects that possess cysteine proteinases. A chimeric gene containing a cDNA clone of rice cystatin (oryzacystatin-I; OC-I), the cauliflower mosaic virus 35S promoter, and the nopaline synthase 3' region was introduced into tobacco plants by Agrobacterium tumefaciens. The presence of the chimeric gene in transgenic plants was detected by a polymerase chain reaction-amplified assay, and transcriptional activity was shown by RNA blot analysis. Heated extracts from transgenic tobacco plants, as well as from progeny which were obtained by selfing a primary transformant, contained protein bands that corresponded in molecular mass to OC-I and reacted with antibodies raised against rOC, a recombinant OC-I protein produced by Escherichia coli. Similar bands were absent in extracts from untransformed control plants. OC-I levels reached 0.5% and 0.6% of the total soluble proteins in leaves and roots, respectively, of some progeny. On a fresh weight basis, the OC-I content was higher in leaves (50 .mu.g/g) than in roots (30 .mu.g/g). OC-I was partially purified from protein extracts of rice seeds and from transgenic tobacco leaves by affinity to anti-rOC antibodies. OC-I from both sources was active against papain.
? ds

Set Items Description
S1 22759 TRANSGENIC?
S2 85262 SEED
S3 187721 MASS
S4 6 S1 AND S2 AND S3
S5 189675 LARGER OR SMALLER
S6 113089 SEED OR SEEDS
S7 6 S1 AND S3 AND S6 NOT S4
? s s1 and s5 and s6 not (s4 or s7)
22759 S1
189675 S5
113089 S6
6 S4
6 S7
S8 12 S1 AND S5 AND S6 NOT (S4 OR S7)
? t s8/7/1-12

8/7/1
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1998 BIOSIS. All rts. reserv.
14221325 BIOSIS Number: 01221325
Somaclonal variation in the progeny of transgenic barley
Bregitzer P; Halbert S E; Lemaux P G
USDA-ARS, Natl. Small Grains Germplasm Res. Facility, P.O. Box 307, Aberdeen, ID 83210, USA
Theoretical and Applied Genetics 96 (3-4). 1998. 421-425.
Full Journal Title: Theoretical and Applied Genetics
ISSN: 0040-5752
Language: ENGLISH
Print Number: Biological Abstracts Vol. 105 Iss. 011 Ref. 148089
Somaclonal variation (SCV) in transgenic plants may slow the incorporation of introduced genes into commercially competitive cultivars. Somaclonal variation in transgenic barley (Hordeum vulgare L.) was assessed in one experiment by comparing the agronomic characteristics of 44 segregating transgenic lines in the T-2 generation to their non-transformed parent ('Golden Promise'). A second experiment examined the agronomic characteristics of seven transgenic-derived, null (non-transgenic) segregant lines in the T-2 and T-4 generations. Compared to their uncultured parent, Golden Promise, most of these lines were shorter, lower yielding, and had smaller seed, and the variability among individual plants was higher. The frequency and severity of the observed SCV was unexpectedly high, and the transformation procedure appeared to induce greater SCV than tissue culture in the absence of transformation. Attempts to understand the sources of SCV, and to modify transformation procedures to reduce the generation of SCV, should be made.

8/7/2
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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13753418 BIOSIS Number: 99753418
Protein processing and auxin response in transgenic tobacco harboring a putative cDNA of zeatin O-xylosyltransferase from Phaseolus vulgaris
Martin R C; Mok M C; Mok D W S
Cent. Gene Res. Biotechnol., Oreg. State Univ., Corvallis, OR 97331-7304, USA
Plant Journal 12 (2). 1997. 305-312.
Full Journal Title: Plant Journal
ISSN: 0960-7412
Language: ENGLISH
Print Number: Biological Abstracts Vol. 104 Iss. 009 Ref. 128199
Zeatin is rapidly metabolized to O-xylosylzeatin in Phaseolus vulgaris seeds. The zeatin O-xylosyltransferase mediating this conversion, a 50 kDa protein, occurs mainly in the endosperm, both in the cytoplasm and the nuclei. A monoclonal antibody specific to the enzyme was used to isolate cDNAs from an expression library derived from P. vulgaris seeds. Two highly homologous, full-length cDNAs were isolated. The ORFs encode proteins of 69 and 67 kDa, respectively, with 90% homology at the amino acid level. cDNA-encoded protein obtained from in vitro transcription/translation was processed to protein of 50 kDa by bean endosperm extract. Transgenic tobacco plants harboring the larger ORF under the control of the CaMV35S promoter were more sensitive to the auxin NAA than control plants. The symptoms included leaf chlorosis, restriction of root elongation, and eventual cessation of growth. The antigenic preprotein was processed, and labeled zeatin was converted to O-xylosylzeatin in transgenic plants grown on NAA-containing medium. Analyses of independently transformed families indicated that the presence of the transgene coincided with the increased auxin sensitivity and protein processing correlated with the manifestation of auxin-induced damage. These results suggest that posttranslational processing regulates enzyme activity, and offer the possibility that cytokinin-auxin balance may be affected by stimulation of cytokinin metabolic enzyme activity by auxin.

8/7/3
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
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13660502 BIOSIS Number: 99660502
Suspensor-derived polyembryony caused by altered expression of valyl-tRNA synthetase in the twn2 mutant of Arabidopsis
Zhang J Z; Somerville C R
Dep. Plant Biol., Carnegie Institution Washington, 290 Panama Strteet, Stanford, CA 94305, USA
Proceedings of the National Academy of Sciences of the United States of America 94 (14). 1997. 7349-7355.
Full Journal Title: Proceedings of the National Academy of Sciences of

the United States of America
ISSN: 0027-8424
Language: ENGLISH
Print Number: Biological Abstracts Vol. 104 Iss. 005 Ref. 068901

The twn2 mutant of Arabidopsis exhibits a defect in early embryogenesis where, following one or two divisions of the zygote, the decendents of the apical cell arrest. The basal cells that normally give rise to the suspensor proliferate abnormally, giving rise to multiple embryos. A high proportion of the seeds fail to develop viable embryos, and those that do, contain a high proportion of partially or completely duplicated embryos. The adult plants are smaller and less vigorous than the wild type and have a severely stunted root. The twn2-1 mutation, which is the only known allele, was caused by a T-DNA insertion in the 5' untranslated region of a putative valyl-tRNA synthetase gene, valRS. The insertion causes reduced transcription of the valRS gene in reproductive tissues and developing seeds but increased expression in leaves. Analysis of transcript initiation sites and the expression of promoter-reporter fusions in transgenic plants indicated that enhancer elements inside the first two introns interact with the border of the T-DNA to cause the altered pattern of expression of the valRS gene in the twn2 mutant. The phenotypic consequences of this unique mutation are interpreted in the context of a model, suggested by Vernon and Meinke (Vernon, D. M. & Meinke, D. W. (1994) Dev. Biol. 165, 566-573), in which the apical cell and its decendents normally suppress the embryogenic potential of the basal cell and its decendents during early embryo development.

8/7/4
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

13497846 BIOSIS Number: 99497846
Food allergens and their modifications by agro-food technology
Moneret-Vautrin D A
Serv. Med. D, Med. Interne Immunologie Clinique Allergologie, Hopital Central, 29 Avenue Marechal-de-Lattre-de-Tassigny, 54035 Nancy Cedex, France
Cahiers Agricultures 6 (1). 1997. 21-29.
Full Journal Title: Cahiers Agricultures
ISSN: 1166-7699
Language: FRENCH
Print Number: Biological Abstracts Vol. 103 Iss. 010 Ref. 136684

Allergens are a special variety of antigens, substances capable of inducing a particular immune response, called "allergic", linked with the synthesis of specific IgEs. This is due to limited protein portions, antigenic determinants or epitopes. Epitopes are generally located at the surface of proteins, in zones of high flexibility and hydrophily. Some epitopes prompt a delayed hypersensibility response, others an IgE or IgG antibody response. There are conformational epitopes (destroyed when the tertiary structure is lost) and sequential epitopes, depending on the aminoacid chain (primary structure). A major allergen is a purified antigen against which at least 50% of tested patients show specific IgE, and which immediately produces positive skin tests, at very low concentration, with at least 90% of subjects having an allergic illness related to this allergen. Isoallergens are molecules with the same molecular weight, identical biological functions (e.g. the same enzymatic activity) and with at least 67% homology to the aminoacid sequence. Allergenic variants are very similar molecule sequences. Natural allergens may undergo posttranscriptional modifications: glycosylation, acylation, methylation, etc. General characteristics of food allergens The molecular weight of most food allergens is between 10,000 and 70,000 Da. Some are larger in size, such as Ara h 1 (63,5 kDa) and Ara h 2 (17 kDa), which exist as polymers of 200 to 300kDa. They are often glycoproteins with an acid isoelectric point. They are hydrosoluble or soluble in saline solution and belong to the family of albumins (soluble in water) or globulins (soluble in saline solution). More rarely they are soluble in alcohol, such as gliadines. They are usually resistant to heat and proteolysis (3, 11-14). Vegetable allergens have been closely studied in recent years. The classical notion of slightly allergenic foods and thermolabile vegetable allergens has been replaced by an inverse concept that allergies to fruits and vegetables are common, with allergens located in aqueous fruits and vegetables, as well as in seeds and particularly in oil-seeds, varying within species and with maturation. Incriminated allergens are proteins that are functionally indispensable and have been preserved in the course of evolution: pan allergens (19-21). Several groups can be distinguished: profilins, PR (pathogenesis-related) proteins (21), enzymes, storage proteins of seeds, stress proteins (heat shock proteins) and Carbohydrate residues (CHD). The conditions of allergenicity depend upon atopy and the characteristics of the responsible protein. The genetic field of atopy, favours the synthesis of specific IgE against environmental antigens. Genetic factors can thus explain why, with respect to the same allergen and identical stimulation conditions, individuals respond with important variations in quantity and affinity of IgE antibodies. Proteins characteristics are: thermic denaturation or resistance; allergen quantity gaining access to mucous membrane; privileged contact of a molecule in sufficient quantity with mucosa; digestibility (enzymatic destruction of food proteins), possibility of a better enterocytic endocytose to favour antigenic presentation to T lymphocytes (hydrophobic proteins such as peanut-oil allergens); existence of crossed reactions between pollinic allergens and vegetable food allergens, so that specific IgE of the first can induce an allergic reaction when they get in contact with the second. This is due to important structural homologies of these pan allergens (19, 20). The incidences of agro-food technologies on allergenicity are the followings: Well-identified risks of food allergy by additives and fabrication auxillaries. These risks are linked to food proteins: caseinates used as texture agents (38), egg lysozyme used as bactericide in cheese fabrication (39), papain, clearing

agent for beers (40L fungic alpha-amylase improving flours (41, 42), fungic lactase added to certain milks (43), etc.; cochineal carmine, a dye for milk products, confectionary, appetizers. (43), vanilla, a flavour forcing its way into a large amount of products (44), etc. Food-storing at ambiant temperature or at + 4 degree C. modification of allergenicity. Role of heating on food reactogenicity. Occurrence of neo-allergens due to heating (46). The allergenic risk of transgenic foods as been considered by the FDA since 1992 (56) and has recently been confirmed for a transgenic soya bean containing the 2S Brazil nut albumin. Introduction of new proteins of bacterial origin in foods for their herbicide-resistance qualities, has already been achieved. There does exist the possibility of de novo allergenicity of these proteins, like the possibility of crossed reactions with bacterial proteins having human tropism. New food proteins. Food allergens are easy objects for various modifications by agro-food technologies. Among them, numerous hydrolysis processes tend to modify the functional qualities of proteins. Besides the fact that hydrolysis does not seem to reduce the risk of reactogenicity (63), we must not forget that most allergens have an average molecular weight of 10 to 40 kDa, and that manufacturing process increasing the quantity of peptides in this weight bracket, could produce neo-allergens. On the contrary, we must consider the possibility of reducing food allergenicity. For instance, there is the whole range of milks, from the milk with partially hydrolysed lactoserum proteins to casein, soy or pork collagen elaborate hydrolysis products, to aminoacid-based milk. Selective depletion of major allergen in a food is already being dealt with for rice and wheat flour (65, 66). There are now increasing interactions between the basic sciences, the medical world and commercial developments.

8/7/5
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

13102959 BIOSIS Number: 99102959
Predicting hybridization between transgenic oilseed rape and wild mustard
Lefol E; Danielou V; Darmency H
Laboratoire de Malherbologie, Institut Natl. de la Recherche Agronomique, BV 1540, 21034 Dijon, France
Field Crops Research 45 (1-3). 1996. 153-161.
Full Journal Title: Field Crops Research
ISSN: 0378-4290
Language: ENGLISH
Print Number: Biological Abstracts Vol. 102 Iss. 005 Ref. 068408
Overlap between flowering of oilseed rape (Brassica napus var. oleifera Metzger) and wild mustard (Sinapis arvensis L.), artificial hybridization between the two species, spontaneous crosses, and backcrossing were assessed to estimate the risk of escape of genes from transgenic crops towards the wild species. In the Burgundy region of France, wild mustard flowers later than oilseed rape. Exposure to cross pollination was two to five times greater with late-flowering cultivars than with early cultivars. Artificial hybridizations using in vitro ovary culture produced up to 1 seed per 100 pollinated flowers. No hybrid was found among 2.9 million seeds produced by wild mustard grown in a garden in presence of a herbicide-resistant transgenic cultivar. No more than six hybrids were obtained from 50 000 flowers of a male-sterile oilseed rape grown in presence of wild mustard. Artificial hybrids grown in presence of wild mustard, or hand-crossed, produced a few aborted seeds. Thus, in similar "normal conditions", it may be concluded that a flower of these two species has a probability smaller than 10-10 of having an interspecific hybrid progeny.

8/7/6
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

11993595 BIOSIS Number: 98593595
Potential persistence of escaped transgenes: Performance of transgenic, oil-modified Brassica seeds and seedlings
Linder C R; Schmitt J
Dep. Biol., Indiana Univ., Bloomington, IN 47405, USA
Ecological Applications 5 (4). 1995. 1056-1068.
Full Journal Title: Ecological Applications
ISSN: 1051-0761
Language: ENGLISH
Print Number: Biological Abstracts Vol. 101 Iss. 002 Ref. 021300
We performed two experiments designed to assess the risk that seed-oil-modification transgenes will increase the persistence of feral Brassica napus canola and interspecific hybrids of B. napus canola and wild Brassica rapa, a weedy relative. The first experiment, conducted at field sites in California and Georgia where oil-modified canola will be grown commercially, tested whether buried seeds of transgenic high-stearate canola had increased survivorship and dormancy. Performance of the high-stearate type was compared to nontransgenic null segregant and parental lines. In California, no differences in initial proportions of dormant seeds and rates of exit could be detected between high-stearate canola and its controls, suggesting low probability that high-stearate canola will form a larger or more persistent seed bank than its nonpersistent controls. In Georgia, although high-stearate canola initially had as low or lower proportions of dormant seeds than its controls, high-stearate seeds exhibited no detectable exit from the seed bank, whereas both controls had significant rates of exit. Hence, escaped high-stearate seed may persist for a longer period than its controls at this site. Differences between the sites highlight the need to conduct risk assessment over the range where a transgenic crop will be commercialized. The second experiment, a greenhouse study, measured the relative ability of oil-modified canolas and wild times crop hybrids to emerge from four depths in the soil (0, 0.5, 4, and 10 cm) and their subsequent seedling vigor. We

tested lines of B. napus canola carrying either the high-stearate gene or a transgene for high-laurate production, using nontransgenic parental types as controls. We also examined the impact of the high-laurate transgene in interspecific wild B. rapa times B. napus canola hybrids. Performance of the high-laurate hybrids was compared to nontransgenic hybrids and the B. rapa wild parent. For all seed types, no seedlings emerged from 10 cm, and all seedlings emerged from 0 and 0.5 cm. A higher proportion of high-stearate canola emerged from 4 cm than its control, but for all depths, high-stearate canola emerged more slowly and had significantly less biomass than its control 2 and 4 wk following emergence. In contrast, high-laurate canola's total emergence and timing of emergence could not be distinguished from its control. Although high-laurate canola's 2-wk biomass was less than that of its control, by 4 wk, its biomass was equivalent due to its significantly higher relative growth rate during that period. The different results for the two oil-modification transgenes suggest that even transgenes with similar functions should be considered on a case-by-case basis. From 0 and 0.5 cm, high-laurate wild times canola hybrids' total emergence, timing of emergence, and biomass accumulation were indistinguishable from their wild parent. High-laurate hybrids emerged more rapidly and had greater biomass at 2 wk than their hybrid controls. Our results indicate that high-laurate hybrids, emerged from shallow depths, may experience performance advantages that will allow them to perform as well as their persistent, wild parent.

8/7/7
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

11987375 BIOSIS Number: 98587375
The phenotypic characterisation of R-2 generation transgenic rice plants under field and glasshouse conditions
Lynch P T; Jones J; Blackhall N W; Davey M R; Power J B; Cocking E C; Nelson M R; Bigelow D M; Orum T V; Orth C E; Schuh W
Plant Biotechnol. Group, Div. Biol. Sci., Univ. Derby, Kedleston Road, Derby DE22 1GB, UK
Euphytica 85 (1-3). 1995. 395-401.
Full Journal Title: Euphytica
ISSN: 0014-2336
Language: ENGLISH
Print Number: Biological Abstracts Vol. 101 Iss. 002 Ref. 015080
The phenotypes of seed progeny (R-2 generation) of Oryza sativa L. cv. Taipei 309, which carried the neomycin phosphotransferase II (npt II) gene, were compared with those of non-transformed, protoplast-derived plants of the same generation and non-transformed, seed-derived plants under field and glasshouse conditions. Under both conditions the transgenic plants were generally smaller, took longer to flower and had reduced fertility. Significant differences were observed between individuals within the group of transgenic plants. The nptII gene was present in most of the transgenic plants, but NPT II activity was only detected in a minority of individuals.

8/7/8
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

11249273 BIOSIS Number: 97449273
Horticultural characteristics of transgenic tobacco expressing the rolC gene from Agrobacterium rhizogenes
Scorza R; Zimmerman T W; Cordts J M; Footen K J; Ravelonandro M
US Dep. Agric.-Agric. Res. Serv., Appalachian Fruit Res. Stn., 45 Wiltshire Rd., Kearneysville, WV 25430, USA
Journal of the American Society for Horticultural Science 119 (5). 1994. 1091-1098.
Full Journal Title: Journal of the American Society for Horticultural Science
ISSN: 0003-1062
Language: ENGLISH
Print Number: Biological Abstracts Vol. 098 Iss. 008 Ref. 103585
Wisconsin 38' tobacco (Nicotiana tabacum L.) leaf discs were transformed with the disarmed Agrobacteium tumefaciens strain EHA101 carrying the rolC gene from A. rhizogenes (Oono et al., 1987) and NPT II and GUS genes. Shoots that regenerated on kanamycin-containing medium were confirmed as transgenic through GUS assays, polymerase chain reaction (PCR), Southern blot analyses, and transmission of the foreign genes through the sexual cycle. Transgenic plants were as short as half the height of control plants; were earlier flowering by up to 35 days; and had smaller leaves, shorter internodes, smaller seed capsules, fewer seeds, smaller flowers, and reduced pollen viability. The number of seed capsules, leaf number, and specific root length were similar between transgenic and control plants. Transgenic clones varied in the expression of the rolC-induced growth alterations as did the first generation of seedlings from these clones. Such differences suggested the potential for selecting for different levels of expression. Transformation with the rolC gene presents a potentially useful method of genetically modifying horticultural crops, particularly for flowering date, height, and leaf and flower size. Chemical names used: neomycin phosphotransferase (NPTII), beta-glucuronidase (GUS).

8/7/9
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

11243575 BIOSIS Number: 97443575
Frequency and distance of pollen dispersal from transgenic oilseed rape (Brassica napus)
Scheffler J A; Parkinson R; Dale P J
Cambridge Lab., AFRC Inst. of Plant Sci. Res., John Innes Centre, Colney, Norwich NR4 7UJ, UK
Transgenic Research 2 (6). 1993. 356-364.

Full Journal Title: Transgenic Research
ISSN: 0962-8819
Language: ENGLISH
Print Number: Biological Abstracts Vol. 098 Iss. 008 Ref. 097887
The objective of this study was to evaluate pollen dispersal in Brassica napus (oilseed rape). The selectable marker, used to follow pollen movement, was a dominant transgene (bar) conferring resistance to the herbicide glufosinate-ammonium. Transgenic and non-transgenic plants of the cultivar Westar were planted in a 1.1 ha field trial, with the transgenic plants in a 9 m diameter circle at the centre, surrounded by non-transgenic plants to a distance of at least 47 m in all directions. A 1 m circle of non-transgenic plants was sown in the centre of the transgenic area to allow estimation of the level of pollen dispersal when plants were in close contact. Honeybee hives were placed at the trial site to optimize the opportunity for cross-pollination. During the flowering period, regular observations were made of the number of plants flowering and the number and type of insects present in 60 1 m-2 areas. These areas were located uniformly around the plot at distances of 1, 3, 6, 12, 24, 36 and 47 m from the edge of the 9 m circle of transgenic plants. Seed samples were harvested from each of the 7 distances so that approximately 20% of the circumference of the plot was sampled at each distance. The centre non-transgenic circle was also sampled. Plants were grown from the seed samples and sprayed with glufosinate to estimate the frequency of pollen dispersal at each distance. In order to screen enough samples to detect low frequency cross-pollination events, seed samples were tested in the greenhouse and on a larger scale in the field. Results were confirmed by testing progeny for glufosinate resistance and by Southern blot analysis. The estimated percentage of pollen dispersal in the non-transgenic centre circle was 4.8%. The frequency was estimated to be 1.5% at a distance of 1 m and 0.4% at 3 m. The frequency decreased sharply to 0.02% at 12 m and was only 0.00033% at 47 m. No obvious directional effects were detected that could be ascribed to wind or insect activity.

8/7/10
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

10126877 BIOSIS Number: 95126877
THE PHENOTYPIC CHARACTERISATION OF R-2 GENERATION TRANSGENIC RICE PLANTS
UNDER FIELD CONDITIONS
SCHUH W; NELSON M R; BIGELOW D M; ORUM T V; ORTH C E; LYNCH P T; EYLES P
S; BLACKHALL N W; JONES J; ET AL
INQ.: M. R. DAVEY, PLANT GENET. MANIPULATION GROUP, DEP. LIFE SCI., UNIV.
NOTTINGHAM, UNIVERSITY PARK, NOTTINGHAM NG7 2RD, UK.
PLANT SCI (LIMERICK) 89 (1). 1993. 69-79. CODEN: PLSCE
Language: ENGLISH
The seed progeny produced by self-pollinating three R1 generation transgenic plants of Oryza sativa L. var. Taipei 309, which carried the neomycin phosphotransferase II (nptII) gene, were grown under field conditions at Maricopa Agricultural Experimental Station, Arizona, USA. The phenotypes of the R2 generation plants were compared with the phenotypes of non-transformed protoplast-derived plants of the same generation and non-transformed seed-derived plants. Transgenic plants were generally smaller with shorter flat leaves, took longer to flower and had reduced fertility. They developed fewer, shorter panicles, with relatively few spikelets which developed into mature seeds. The seeds from the transgenic plants were longer, but narrower than those produced by non-transformed plants. Significant phenotypic differences were observed between individuals within the group of R2 transgenic plants. The nptII gene was present in all transgenic plants, but the NPT II enzyme was not detected.

8/7/11
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

7407845 BIOSIS Number: 89058864
ENHANCEMENT OF THE METHIONINE CONTENT OF SEED PROTEINS BY THE EXPRESSION
OF A CHIMERIC GENE ENCODING A METHIONINE-RICH PROTEIN IN TRANSGENIC PLANTS
ALTENBACH S B; PEARSON K W; MEEKER G; STARACI L C; SUN S S M
PLANT CELL RES. INST. INC., 6560 TRINITY COURT, DUBLIN, CALIF. 94568, USA.
PLANT MOL BIOL 13 (5). 1989. 513-522. CODEN: PMBID
Full Journal Title: Plant Molecular Biology
Language: ENGLISH
We have constructed a chimeric gene encoding a Brazil nut methionine-rich seed protein which contains 18% methionine. This gene has been transferred to tobacco and expressed in the developing seeds. Tobacco seeds are able to process the methionine-rich protein efficiently from a larger precursor polypeptide of 17 kDa to the 9 kDa and 3 kDa subunits of the mature protein, a procedure which involves three proteolytic cleavage steps in the Brazil nut seed. The accumulation of the methionine-rich protein in the seeds of tobacco results in a significant increase (30%) in the levels of the methionine in the seed proteins of the transgenic plants. Our data indicate that the introduction of a chimeric gene encoding a methionine-rich seed protein into crop plants, particularly legumes whose seeds are deficient in the essential sulfur-containing amino acids, represents a feasible method for improving the nutritional quality of seed proteins.

8/7/12
DIALOG(R)File 5:BIOSIS PREVIEWS(R)

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6987569 BIOSIS Number: 87048090
THE SEQUENCE OF A PEA VICILIN GENE AND ITS EXPRESSION IN TRANSGENIC
TOBACCO PLANTS
HIGGINS T J V; NEWBIGIN E J; SPANCER D; LLEWELLYN D J; CRAIG S
CSIRO, DIV. PLANT INDUSTRY, GPO BOX 1600, CANBERRA 2601, AUST.
PLANT MOL BIOL 11 (5). 1988. 683-696. CODEN: PMBID
Full Journal Title: Plant Molecular Biology
Language: ENGLISH
A 5.5 kb Eco RI fragment containing a vicilin gene was selected from a Pisum sativum genomic library, and the protein-coding region and adjacent 5' and 3' regions were sequenced. A DNA construction comprising this 5.5 kb fragment together with a gene for neomycin phosphotransferase II was stably introduced into tobacco using an Agrobacterium tumefaciens binary vector, and the fidelty of expression of the pea vicilin gene in its new host was studied. The seeds of eight transgenic tobacco plants showed a sixteen-fold range in the level of accumulated pea vicilin. The level of accumulation of vicilin protein and mRNA correlated with the numbers of integrated copies of the vicilin gene. Pea vicilin was confined to the seeds of transgenic tobacco. Using immunogold labelling, vicilin was detected in protein bodies of eight out of ten embryos (axes plus cotyledons) and, at a much lower level, in two out of eleven endosperms. Pea vicilin was synthesized early in tobacco seed development; some molecules were cleaved as is the case in pea seeds, yielding a major parental component of Mr .apprx. 50,000 together with a range of smaller polypeptides.
? s seed (w)size
85262 SEED
280858 SIZE
S9 2255 SEED (W)SIZE
? ds

Set Items Description
S1 22759 TRANSGENIC?
S2 85262 SEED
S3 187721 MASS
S4 6 S1 AND S2 AND S3
S5 189675 LARGER OR SMALLER
S6 113089 SEED OR SEEDS
S7 6 S1 AND S3 AND S6 NOT S4
S8 12 S1 AND S5 AND S6 NOT (S4 OR S7)
S9 2255 SEED (W)SIZE
? s s1 and s9
22759 S1
2255 S9
S10 2 S1 AND S9
? t s10/7/1 2

10/7/1
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1998 BIOSIS. All rts. reserv.
11675196 BIOSIS Number: 98275196
Molecular genetic analysis of subterranean clover-microbe interactions
Rolfe B G; Djordjevic M A; Weinman J J; McIver J; Gartner E; Chen H; Creaser E H; Britt K; Lawson C G R; De Boer M H; McKay I A; Shoobridge M V; De Majnik J; Pittock C; Broderick K; Delbridge T
Cent. Genetic Res., Plant-Microbe Interaction Group, Res. Sch. Biol. Sci., Australian National University, PO Box 475, Canberra, ACT 2601, Australia
Soil Biology and Biochemistry 27 (4-5). 1995. 485-490.
Full Journal Title: Soil Biology and Biochemistry
ISSN: 0038-0717
Language: ENGLISH
Print Number: Biological Abstracts Vol. 100 Iss. 001 Ref. 000034
Trifolium subterraneum (subterranean clover) is of considerable economic importance to the Australian rural industries as a pasture legume. In addition to its commercial value, it has a number of specific attributes-such as small seed size, diploidy, self-fertilization, the ability to be transformed and small genome-which make it a prime target for the modern techniques of molecular genetics. We report genetic and physiological factors that control the production and excretion of the lipooligosaccharide molecules formed by Rhizobium leguminosarum bv. trifolii in the formation of the symbiosis with subterranean clover. These molecules, synthesized by the products of the nodulation (nod) genes, are a major determinant of nodule occupancy and the strain selection imposed by the host plant. In addition, we have investigated which plant genes and proteins are activated in subterranean clover when they are either physically wounded, infected with Rhizobium, or attacked by red-legged earth mites. To analyse these interactions more precisely, we have cloned plant genes involved in the phenylpropanoid pathway and used their promoters to construct transgenic subterranean clover plants. Our studies provide an insight into the nature and consequences of the chemical exchange between plants and invading microbes.

10/7/2
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1998 BIOSIS. All rts. reserv.
9333800 BIOSIS Number: 43078800
HORTICULTURAL CHARACTERISTICS OF TRANSGENIC TOBACCO EXPRESSING THE ROL C
GENE FROM AGROBACTERIUM-RHIZOGENES
SCORZA R; ZIMMERMAN T W; CORDTS J M; FOOTEN K J; RAVELONANDRO M
USDA-APPALACHIAN FRUIT RES. STATION, KEARNEYSVILLE, WEST VA.
89TH ANNUAL MEETING OF THE AMERICAN SOCIETY FOR

HORTICULTURAL SCIENCE,
HONOLULU, HAWAII, USA, JULY 30-AUGUST 6, 1992. HORTSCIENCE 27 (6).
1992.
621. CODEN: HJHSA
Language: ENGLISH
? t s10/5/2

10/5/2
DIALOG(R)File 5:BIOSIS PREVIEWS(R)
(c) 1998 BIOSIS. All rts. reserv.
9333800 BIOSIS Number: 43078800
HORTICULTURAL CHARACTERISTICS OF TRANSGENIC TOBACCO
EXPRESSING THE ROL C
GENE FROM AGROBACTERIUM-RHIZOGENES
SCORZA R; ZIMMERMAN T W; CORDTS J M; FOOTEN K J; RAVELONANDRO
M
USDA-APPALACHIAN FRUIT RES. STATION, KEARNEYSVILLE, WEST VA.
89TH ANNUAL MEETING OF THE AMERICAN SOCIETY FOR
HORTICULTURAL SCIENCE,
HONOLULU, HAWAII, USA, JULY 30-AUGUST 6, 1992. HORTSCIENCE 27 (6).
1992.
621. CODEN: HJHSA
Language: ENGLISH
Document Type: CONFERENCE PAPER
Descriptors/Keywords: ABSTRACT NICOTIANA-TABACUM PLANT CROP
INDUSTRY
BACTERIA MICROORGANISM GROWTH HEIGHT FLOWERING DATE SEED
SIZE ROOT
DENSITY
Concept Codes:
*03504 Genetics and Cytogenetics-Plant
*31500 Genetics of Bacteria and Viruses
*51510 Plant Physiology, Biochemistry and Biophysics-Growth,
Differentiation
*51512 Plant Physiology, Biochemistry and Biophysics-Reproduction
*52512 Agronomy-Tobacco Crops
00520 General Biology-Symposia, Transactions and Proceedings of
Conferences, Congresses, Review Annuals
51000 Morphology, Anatomy and Embryology of Plants
Biosystematic Codes:
06509 Rhizobiaceae (1992-)
26775 Solanaceae
Super Taxa:
Microorganisms; Bacteria; Eubacteria; Plants; Vascular Plants;
Spermatophytes; Angiosperms; Dicots
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$0.19 Estimated cost this search
$0.19 Estimated total session cost 0.059 DialUnits

File 351:DERWENT WPI 1963-1998/UD=9824;UP=9821;UM=9819
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*File 351: Some images missing from UD=9816-9819 to be added as soon as possible. Output formats changed for 1998. See HELP FORM 351 for info.

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WPI Acc No: 98-179060/199816
Title Terms: DOMAIN; CONTAIN; NUCLEIC; ACID; PRODUCE; PLANT; MODULATE; SEED
; MASS; INCREASE; PROTEIN; CARBOHYDRATE; OIL; CONTENT; SEED; PLANT
Index Terms/Additional Words: APETALA; 2; FLORAL; HOMEOTIC; GENE
? t s1/7

1/7/1
DIALOG(R)File 351:DERWENT WPI
(c)1998 Derwent Info Ltd. All rts. reserv.
011762150
WPI Acc No: 98-179060/199816
Use of AP2 domain containing nucleic acid(s) - for producing plants with modulated seed mass, e.g. increased protein, carbohydrate or oil content, or seedless plants
Patent Assignee: UNIV CALIFORNIA (REGC)
Inventor: JOFUKU K D; OKAMURO J K
Number of Countries: 078 Number of Patents: 001
Patent Family:
Patent No Kind Date Applicat No Kind Date Main IPC Week
WO 9807842 A1 19980226 WO 97US14659 A 19970819 C12N-015/00 199816 B
Priority Applications (No Type Date): US 97879827 A 19970620; US 96700152 A 19960820
Patent Details:
Patent Kind Lan Pg Filing Notes Application Patent
WO 9807842 A1 E 68
Designated States (National): AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA
UG US UZ VN YU ZW
Designated States (Regional): AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW
Abstract (Basic): WO 9807842 A

A method of modulating seed mass in a plant comprises: (a) providing a first plant comprising a recombinant expression cassette containing an AP2 domain containing (ADC) nucleic acid linked to a plant promoter; (b) selfing the first plant or crossing the first plant with a second plant, thereby producing seeds; and (c) selecting seed with altered mass.

Also claimed are: (1) a seed comprising a recombinant expression cassette containing an ADC nucleic acid; (2) a transgenic plant comprising an expression cassette containing a plant promoter operably linked to a heterologous ADC polynucleotide; and (3) an isolated nucleic acid molecule comprising an expression cassette containing a plant promoter operably linked to a heterologous ADC polynucleotide.

USE - AP2 (APETALA2) is a floral homeotic gene of Arabidopsis that controls three critical aspects of flower ontogeny: the establishment of the floral meristem, the specification of floral organ identity and the temporal and spatial regulation of floral homeotic gene expression.

The products can be used for producing plants with improved traits, e.g. producing seeds with increased protein content, carbohydrate content or oil content, or producing seedless varieties of crop plants.

Dwg.0/6
Derwent Class: C06; D16; P13
International Patent Class (Main): C12N-015/00
International Patent Class (Additional): A01H-001/00; A01H-005/00; A01H-005/10; C12N-015/29
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$3.35 2 Types
$13.10 Estimated cost File351
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$13.29 Estimated total session cost 1.059 DialUnits
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